



642669

SEQUENCE LISTING

<110> CONSEJO SUPERIOR DE INVESTIGACIONES CIENTIFICAS
BIONOSTRA, S.L.

<120> CHIMERIC EMPTY CAPSIDS OF THE INFECTIOUS BURSAL DISEASE VIRUS (IBDV),
OBTAINMENT PROCESS AND APPLICATIONS

<130> 7572-73329-01

<140> US 10/579,428

<141> 2006-05-12

<150> ES P200400120

<151> 2004-01-21

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<170> PatentIn version 3.1

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Met Trp Leu Glu Glu Asn Gly Ile Val Thr Asp Met Ala Asn Phe Ala		
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Pro Gln Ala Gly Ser Lys Ser Gln Arg Ala Lys Tyr Gly Thr Ala Gly		
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Tyr Gly Val Glu Ala Arg Gly Pro Thr Pro Glu Glu Ala Gln Arg Glu		
85 90 95 100		
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Lys Asp Thr Arg Ile Ser Lys Lys Met Glu Thr Met Gly Ile Tyr Phe		
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Gly Gln Val Lys Tyr Trp Gln Asn Lys Arg Glu Ile Pro Asp Pro Asn		
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gag gac tat cta gac tac gtg cat gca gag aag agc cgg ttg gca tca	8577	
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Glu Glu Gln Ile Leu Arg Ala Ala Thr Ser Ile Tyr Gly Ala Pro Gly		
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Gln Ala Glu Pro Pro Gln Ala Phe Ile Asp Glu Val Ala Lys Val Tyr		
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ctc ttg act gcg atg gag atg aag cat cgc aat ccc agg cgg gct cta Leu Leu Thr Ala Met Glu Met Lys His Arg Asn Pro Arg Arg Ala Leu 215 220 225	8769
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cgg ctg ggc cgc tgg atc agg acc gtc tct gat gag gac ctt gag gga Arg Leu Gly Arg Trp Ile Arg Thr Val Ser Asp Glu Asp Leu Glu Gly 245 250 255 260	8865
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<212> PRT
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35 40 45
Ala Asn Phe Ala Leu Ser Asp Pro Asn Ala His Arg Met Arg Asn Phe
50 55 60
Leu Ala Asn Ala Pro Gln Ala Gly Ser Lys Ser Gln Arg Ala Lys Tyr
65 70 75 80
Gly Thr Ala Gly Tyr Gly Val Glu Ala Arg Gly Pro Thr Pro Glu Glu
85 90 95
Ala Gln Arg Glu Lys Asp Thr Arg Ile Ser Lys Lys Met Glu Thr Met
100 105 110
Gly Ile Tyr Phe Ala Thr Pro Glu Trp Val Ala Leu Asn Gly His Arg
115 120 125
Gly Pro Ser Pro Gly Gln Val Lys Tyr Trp Gln Asn Lys Arg Glu Ile
130 135 140
Pro Asp Pro Asn Glu Asp Tyr Leu Asp Tyr Val His Ala Glu Lys Ser
145 150 155 160
Arg Leu Ala Ser Glu Glu Gln Ile Leu Arg Ala Ala Thr Ser Ile Tyr
165 170 175
Gly Ala Pro Gly Gln Ala Glu Pro Pro Gln Ala Phe Ile Asp Glu Val
180 185 190

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Ala Lys Val Tyr Glu Ile Asn His Gly Arg Gly Pro Asn Gln Glu Gln
195 200 205

Met Lys Asp Leu Leu Leu Thr Ala Met Glu Met Lys His Arg Asn Pro
210 215 220

Arg Arg Ala Leu Pro Lys Pro Lys Pro Lys Pro Asn Ala Pro Thr Gln
225 230 235 240

Arg Pro Pro Gly Arg Leu Gly Arg Trp Ile Arg Thr Val Ser Asp Glu
245 250 255

Asp Leu Glu Gly Ser Ile Ala Thr Met Val Ser Lys Gly Glu Glu Leu
260 265 270

Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn
275 280 285

Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr
290 295 300

Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
305 310 315 320

Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe
325 330 335

Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala
340 345 350

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
355 360 365

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
370 375 380

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
385 390 395 400

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
405 410 415

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
420 425 430

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
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Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
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Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
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Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
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<211> 33
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33

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gtc tat gaa atc aac cat gga cgt ggc cca aac caa gaa cag atg aaa Val Tyr Glu Ile Asn His Gly Arg Gly Pro Asn Gln Glu Gln Met Lys 235 240 245		893
gat ctg ctc ttg act gcg atg gag atg aag cat cgc aat ccc agg cgg Asp Leu Leu Leu Thr Ala Met Glu Met Lys His Arg Asn Pro Arg Arg 250 255 260 265		941
gct cta cca aag ccc aag cca aaa ccc aat gct cca aca cag aga ccc Ala Leu Pro Lys Pro Lys Pro Asn Ala Pro Thr Gln Arg Pro 270 275 280		989
cct ggt cg ^g ctg ggc cgc tgg atc agg acc gtc tct gat gag gac ctt Pro Gly Arg Leu Gly Arg Trp Ile Arg Thr Val Ser Asp Glu Asp Leu 285 290 295		1037
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gc	ag	ac	ag	cg	ta	ac	ct	tt	tc	ac	cc	tg	4273
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Ser Ala Glu Gln Ile Ala Ala Met Ala Ala Ser Glu Phe Lys Glu Thr
35 40 45

Pro Glu Leu Glu Ser Ala Val Arg Ala Met Glu Ala Ala Ala Asn Val
50 55 60

Asp Pro Leu Phe Gln Ser Ala Leu Ser Val Phe Met Trp Leu Glu Glu
65 70 75 80

Asn Gly Ile Val Thr Asp Met Ala Asn Phe Ala Leu Ser Asp Pro Asn
85 90 95

Ala His Arg Met Arg Asn Phe Leu Ala Asn Ala Pro Gln Ala Gly Ser
100 105 110

Lys Ser Gln Arg Ala Lys Tyr Gly Thr Ala Gly Tyr Gly Val Glu Ala
115 120 125

Arg Gly Pro Thr Pro Glu Glu Ala Gln Arg Glu Lys Asp Thr Arg Ile
130 135 140

Ser Lys Lys Met Glu Thr Met Gly Ile Tyr Phe Ala Thr Pro Glu Trp
145 150 155 160

Val Ala Leu Asn Gly His Arg Gly Pro Ser Pro Gly Gln Val Lys Tyr
165 170 175

Trp Gln Asn Lys Arg Glu Ile Pro Asp Pro Asn Glu Asp Tyr Leu Asp
180 185 190

Tyr Val His Ala Glu Lys Ser Arg Leu Ala Ser Glu Glu Gln Ile Leu
195 200 205

Arg Ala Ala Thr Ser Ile Tyr Gly Ala Pro Gly Gln Ala Glu Pro Pro
210 215 220

Gln Ala Phe Ile Asp Glu Val Ala Lys Val Tyr Glu Ile Asn His Gly
225 230 235 240

Arg Gly Pro Asn Gln Glu Gln Met Lys Asp Leu Leu Leu Thr Ala Met
245 250 255

Glu Met Lys His Arg Asn Pro Arg Arg Ala Leu Pro Lys Pro Lys Pro
260 265 270

Lys Pro Asn Ala Pro Thr Gln Arg Pro Pro Gly Arg Leu Gly Arg Trp
275 280 285

Ile Arg Thr Val Ser Asp Glu Asp Leu Glu
290 295

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